RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/586, 229_
Source: _1FwP_
Date Processed by STIC: _7/26/06_

ENTERED

RAW SEQUENCE LISTING   DATE: 07/26/2006
PATENT APPLICATION: US/10/586,229   TIME: 14:17:48

Input Set : A:\50274.021003.SEQLIST.TXT
Output Set: N:\CRF4\07262006\J586229.raw

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   4 <110> APPLICANT: VOLLMERS, Heinz Peter
   5        MUELLER-HERMELINK, Hans Konrad
   6        HENSEL, Frank
   8 <120> TITLE OF INVENTION: Neoplasm-Specific Polypeptides and Their
   9        Uses
  11 <130> FILE REFERENCE: 50274/021003
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/586,229
C--> 13 <141> CURRENT FILING DATE: 2006-07-19
  13 <150> PRIOR APPLICATION NUMBER: PCT/US05/02480
  14 <151> PRIOR FILING DATE: 2005-01-26
  16 <150> PRIOR APPLICATION NUMBER: US 10/764,730
  17 <151> PRIOR FILING DATE: 2004-01-26
  19 <160> NUMBER OF SEQ ID NOS: 30
  21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  23 <210> SEQ ID NO: 1
  24 <211> LENGTH: 288
  25 <212> TYPE: DNA
  26 <213> ORGANISM: Mus musculus
  28 <220> FEATURE:
  29 <221> NAME/KEY: CDS
  30 <222> LOCATION: (1)...(288)
  32 <400> SEQUENCE: 1
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  34 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp
  35  1               5                  10                  15
  37 gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag att tat      96
  38 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
  39              20                  25                  30
  41 cct gga agt ggt aat act tac tac aat gag aag ttc aag ggc aag gcc     144
  42 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
  43          35                  40                  45
  45 aca ctg act gca gac aaa tcc tcc agc aca gcc tac atg cag ctc agc     192
  46 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
  47      50                  55                  60
  49 agc ctg aca tct gag gac tct gca gtc tat ttc tgt gca aga tcg gga     240
  50 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
  51  65                  70                  75                  80
  53 tta cga ccc tat gct atg gac tac tgg ggt caa gga acc tca gtc acc     288
  54 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
  55              85                  90                  95
  59 <210> SEQ ID NO: 2
  60 <211> LENGTH: 96
  61 <212> TYPE: PRT
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62 <213> ORGANISM: Mus musculus
64 <400> SEQUENCE: 2
65 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp
66  1               5                  10                  15
67 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
68            20                  25                  30
69 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
70          35                  40                  45
71 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
72      50                  55                  60
73 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
74 65                  70                  75                  80
75 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
76              85                  90                  95
79 <210> SEQ ID NO: 3
80 <211> LENGTH: 315
81 <212> TYPE: DNA
82 <213> ORGANISM: Mus musculus
84 <220> FEATURE:
85 <221> NAME/KEY: CDS
86 <222> LOCATION: (1)...(315)
88 <400> SEQUENCE: 3
89 cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc   48
90 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
91  1               5                  10                  15
93 aga tct agt cag agc att gta cat agt aat gga aac acc tat tta gaa   96
94 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
95            20                  25                  30
97 tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg atc tac aaa  144
98 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
99          35                  40                  45
101 gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga  192
102 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
103          50                  55                  60
105 tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat  240
106 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
107 65                  70                  75                  80
109 ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt ccg tac acg ttc  288
110 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
111              85                  90                  95
113 gga ggg ggg acc aag ctg gaa ata aaa                              315
114 Gly Gly Gly Thr Lys Leu Glu Ile Lys
115              100                 105
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 105
120 <212> TYPE: PRT
121 <213> ORGANISM: Mus musculus
123 <400> SEQUENCE: 4
124 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
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125  1                    5                     10                    15
126  Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
127          20                    25                    30
128  Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
129          35                    40                    45
130  Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
131          50                    55                    60
132  Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
133  65                    70                    75                    80
134  Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
135                    85                    90                    95
136  Gly Gly Gly Thr Lys Leu Glu Ile Lys
137                    100                   105
140  <210> SEQ ID NO: 5
141  <211> LENGTH: 3114
142  <212> TYPE: DNA
143  <213> ORGANISM: Homo sapiens
145  <220> FEATURE:
146  <221> NAME/KEY: CDS
147  <222> LOCATION: (1)...(3114)
149  <400> SEQUENCE: 5
150  gat gtg agg gag cct gaa aat gaa att tct tca gac tgc aat cat ttg    48
151  Asp Val Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu
152  1                    5                     10                    15
154  ttg tgg aat tat aag ctg aac cta act aca gat ccc aaa ttt gaa tct    96
155  Leu Trp Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser
156                    20                    25                    30
158  gtg gcc aga gag gtt tgc aaa tct act ata aca gag att gaa gaa tgt   144
159  Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Glu Glu Cys
160          35                    40                    45
162  gct gat gaa ccg gtt gga aaa ggt tac atg gtt tcc tgc ttg gtg gat   192
163  Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp
164          50                    55                    60
166  cac cga ggc aac atc act gag tat cag tgt cac cag tac att acc aag   240
167  His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys
168  65                    70                    75                    80
170  atg acg gcc atc att ttt agt gat tac cgt tta atc tgt ggc ttc atg   288
171  Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met
172                    85                    90                    95
174  gat gac tgc aaa aat gac atc aac att ctg aaa tgt ggc agt att cgg   336
175  Asp Asp Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg
176                    100                   105                   110
178  ctt gga gaa aag gat gca cat tca caa ggt gag gtg gta tca tgc ttg   384
179  Leu Gly Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu
180          115                   120                   125
182  gag aaa ggc ctg gtg aaa gaa gca gaa gaa aga gaa ccc aag att caa   432
183  Glu Lys Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln
184          130                   135                   140
186  gtt tct gaa ctc tgc aag aaa gcc att ctc cgg gtg gct gag ctg tca   480
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187 Val Ser Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser
188 145               150               155               160
190 tcg gat gac ttt cac tta gac cgg cat tta tat ttt gct tgc cga gat   528
191 Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp
192               165               170               175
194 gat cgg gag cgt ttt tgt gaa aat aca caa gct ggt gag ggc aga gtg   576
195 Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val
196               180               185               190
198 tat aag tgc ctc ttt aac cat aaa ttt gaa gaa tcc atg agt gaa aag   624
199 Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys
200               195               200               205
202 tgt cga gaa gca ctt aca acc cgc caa aag ctg att gcc cag gat tat   672
203 Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr
204       210               215               220
206 aaa gtc agt tat tca ttg gcc aaa tcc tgt aaa agt gac ttg aag aaa   720
207 Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys
208 225               230               235               240
210 tac cgg tgc aat gtg gaa aac ctt ccg cga tcg cgt gaa gcc agg ctc   768
211 Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu
212               245               250               255
214 tcc tac ttg tta atg tgc ctg gag tca gct gta cac aga ggg cga caa   816
215 Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln
216               260               265               270
218 gtc agc agt gag tgc cag ggg gag atg ctg gat tac cga cgc atg ttg   864
219 Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu
220               275               280               285
222 atg gaa gac ttt tct ctg agc cct gag atc atc cta agc tgt cgg ggg   912
223 Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly
224       290               295               300
226 gag att gaa cac cat tgt tcc gga tta cat cga aaa ggg cgg acc cta   960
227 Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu
228 305               310               315               320
230 cac tgt ctg atg aaa gta gtt cga ggg gag aag ggg aac ctt gga atg   1008
231 His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met
232               325               330               335
234 aac tgc cag cag gcg ctt caa aca ctg att cag gag act gac cct ggt   1056
235 Asn Cys Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly
236               340               345               350
238 gca gat tac cgc att gat cga gct ttg aat gaa gct tgt gaa tct gta   1104
239 Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val
240               355               360               365
242 atc cag aca gcc tgc aaa cat ata aga tct gga gac cca atg atc ttg   1152
243 Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu
244       370               375               380
246 tcg tgc ctg atg gaa cat tta tac aca gag aag atg gta gaa gac tgt   1200
247 Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys
248 385               390               395               400
250 gaa cac cgt ctc tta gag ctg cag tat ttc atc tcc cgg gat tgg aag   1248
251 Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys
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252                405                410                415
254 ctg gac cct gtc ctg tac cgc aag tgc cag gga gac gct tct cgt ctt   1296
255 Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu
256             420                425                430
258 tgc cac acc cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga   1344
259 Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly
260             435                440                445
262 gct gtg ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag   1392
263 Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln
264     450                455                460
266 gga agg agg ctc tca cgg gag tgc cga gct gaa gtc caa agg atc cta   1440
267 Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu
268 465                470                475                480
270 cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat aag   1488
271 His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys
272             485                490                495
274 tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag act gga   1536
275 Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly
276         500                505                510
278 cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta gtg gtg gag   1584
279 Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu
280         515                520                525
282 tgt aga gat ata gtt ggc aac ctc act gag tta gaa tca gag gat att   1632
283 Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile
284     530                535                540
286 caa ata gaa gcc ttg ctg atg aga gcc tgt gag ccc ata att cag aac   1680
287 Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn
288 545                550                555                560
290 ttc tgc cac gat gtg gca gat aac cag ata gac tcc ggg gac ctg atg   1728
291 Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met
292             565                570                575
294 gag tgt ctg ata cag aac aaa cac cag aag gac atg aac gag aag tgt   1776
295 Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys
296         580                585                590
298 gcc atc gga gtt acc cac ttc cag ctg gtg cag atg aag gat ttt cgg   1824
299 Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg
300         595                600                605
302 ttt tct tac aag ttt aaa atg gcc tgc aag gag gac gtg ttg aag ctt   1872
303 Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu
304     610                615                620
306 tgc cca aac ata aaa aag aag gtg gac gtg gtg atc tgc ctg agc acg   1920
307 Cys Pro Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr
308 625                630                635                640
310 acc gtg cgc aat gac act ctg cag gaa gcc aag gag cac agg gtg tcc   1968
311 Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser
312             645                650                655
314 ctg aag tgc cgc agg cag ctc cgt gtg gag gag ctg gag atg acg gag   2016
315 Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu
316     660                665                670
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1059 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:1057
L:1099 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:1097